+FGF-1
[HUVEC]
migratory
proliferative
non-polar
~60 PD's
non-migratory
non-proliferative
[HUVEC]
senescent giant cell
INF-γ
IL-1,INF
TGF-β,PMA
[HUVEC]
migratory
non-proliferative
polar
[HUVEC]
migratory
aligned
[HUVEC]
migratory
branched
Trypsin +
FGF-1
[HUVEC]
organized

FIG. 1

Domain Structure of the Notch Ligand Family

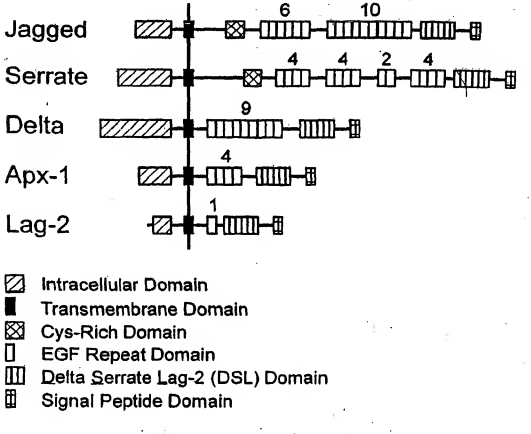


FIG. 2

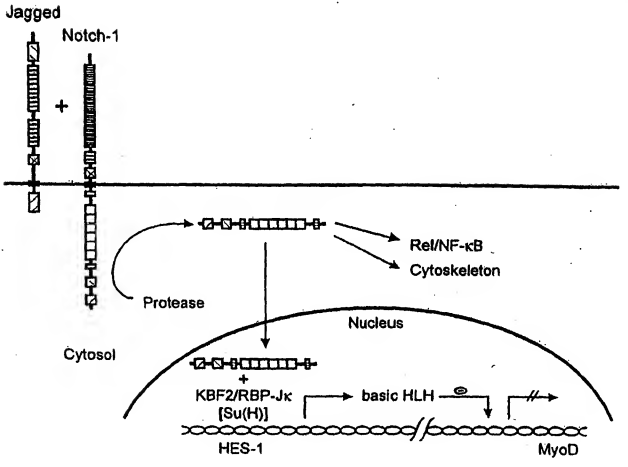
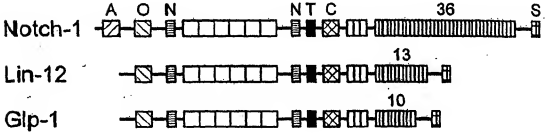

Jagged
Notch-1
+
Rel/NF-κB
Cytoskeleton
Protease
Nucleus
Cytosol
+
KBF2/RBP-Jκ
[Su(H)]
basic HLH
HES-1
MyoD

FIG. 3

Domain Structure of the Notch Receptor Family



- Transmembrane Domain (T)
- Cys-Rich Domain (Notch Lin Glp Repeats, NLG)
- Ankyrin Repeat Domain
- Proline Glutamate Serine Threonine (PEST) Domain (A)
- Polyglutamine-Rich (OPA) Domain (O)
- Nuclear Localization Signal Domain (N)
- Cys-Poor Domain (C)
- EGF Repeat Domain
- Signal Peptide Sequence (S)

FIG.4

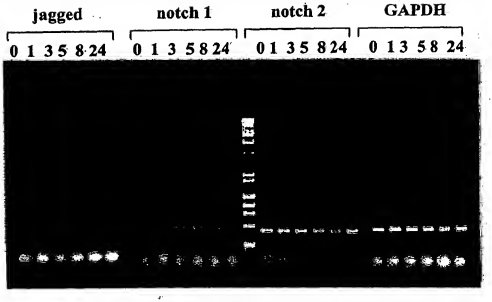

jagged
notch 1
notch 2
GAPDH
0 1 3 5 8 24
0 1 3 5 8 24
0 1 3 5 8 24
0 1 3 5 8 24

FIG. 5

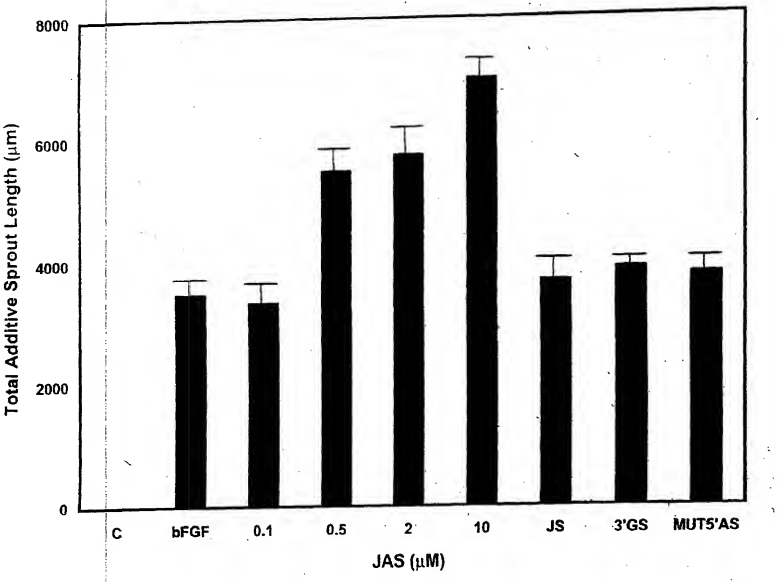

8000
6000
4000
2000
0
Total Additive Sprout Length (μm)
C
bFGF
0.1
0.5
2
10
JS
3'GS
MUT5'AS
JAS (μM)

FIG. 6

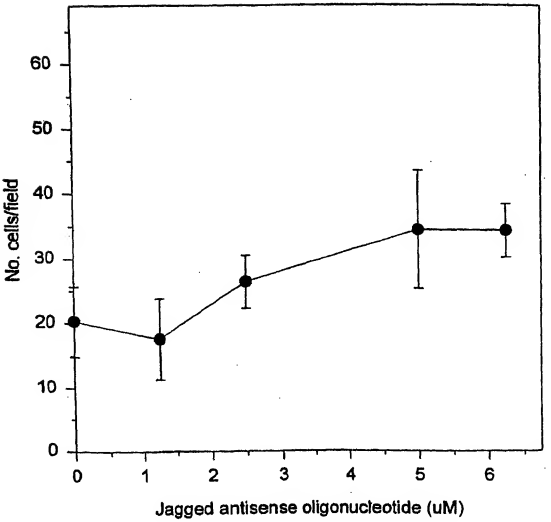

No. cells/field
60
50
40
30
20
10
0
0
1
2
3
4
5
6
Jagged antisense oligonucleotide (uM)

FIG. 7A

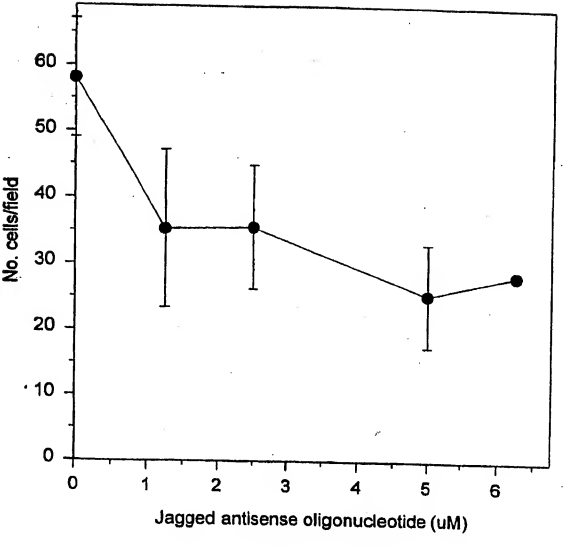

No. cells/field
60
50
40
30
20
10
0
0
1
2
3
4
5
6
Jagged antisense oligonucleotide (uM)

FIG. 7B

```
1    MRSPRTRGRS GRPLSLLLAL LCALRAKVCG ASGQFELEIL SMQNVNGELQ
51   NGNCCGGARN PGDRKCTRDE CDTYFKVCLK EYQSRVTAGG PCSFGSGSTP
101  VIGGNTFNLK ASRGNDRNRI VLPFSFAWPR SYTLLVEAWD SSNDTVQPDS
151  IIEKASHSGM INPSRQWQTL KQNTGVAHFE YQIRVTCDDY YYGFGCNKFC
201  RPRDDFFGHY ACDQNGNKTC MEGWMGPECN RAICRQGCSP KHGSCKLPGD
251  CRCQYGWQGL YCDKCIPHPG CVHGICNEPW QCLCETNWGG QLCDKDLNYC
301  GTHQPCLNGG TCSNTGPDKY QCSCPEGYSG PNCEIAEHAC LSDPCHNRGS
351  CKETSLGFEC ECSPGWTGPT CSTNIDDCSP NNCSHGGTCQ DLVNGFKCVC
401  PPQWTGKTCQ LDANECEAKP CVNAKSCKNL IASYYCDCLP GWMGQNCDIN
451  INDCLGQCQN DASCRDLVNG YRCICPPGYA GDHCERDIDE CASNPCLNGG
501  HCQNEINRFQ CLCPTGFSGN LCQLDIDYCE PNPCQNGAQC YNRASDYFCK
551  CPEDYEGKNC SHLKDHCRTT PCEVIDSCTV AMASNDTPEG VRYISSNVCG
601  PHGKCKSQSG GKFTCDCNKG FTGTYCHENI NDCESNPCRN GGTCIDGVNS
651  YKCICSDGWE GAYCETNIND CSQNPCHNGG TCRDLVNDFY CDCKNGWKGK
701  TCHSRDSQCD EATCNNGGTC YDEGDAFKCM CPGGWEGTTC NIARNSSCLP
751  NPCHNGGTCV VNGESFTCVC KEGWEGPICA QNTNDCSPHP CYNSGTCVDG
801  DNWYRCECAP GFAGPDCRIN INECQSSPCA FGATCVDEIN GYRCVCPPGH
851  SGAKCQEVSG RPCITMGSVI PDGAKWDDDC NTCQCLNGRI ACSKVWCGPR
901  PCLLHKGHSE CPSGQSCIPI LDDQCFVHPC TGVGECRSSS LQPVKTKCTS
951  DSYYQDNCAN ITFTFNKEMM SPGLTTEHIC SELRNLNILK NVSAEYSIYI
1001 ACEPSPSANN EIHVAISAED IRDDGNPIKE ITDKIIDLVS KRDGNSSLIA
1051 AVAEVRVQRR PLKNRTDFLV PLLSSVLTVA WICCLVTAFY WCLRKRRKPG
1101 SHTHSASEDN TTNNVREQLN QIKNPIEKHG ANTVPIKDYE NKNSKMSKIR
1151 THNSEVEEDD MDKHQQKARF GKQPAYTLVD REEKPPNGTP TKHPNWTNKQ
1201 DNRDLESAQS LNRMEYIV
```

FIG. 8A

```
1     ATGCGTTCCC CACGGACRCG CGGCCGGTCC GGGCGCCCCC TAAGCCTCCT
51    GCTCGCCCTG CTCTGTGCCC TGCGAGCCAA GGTGTGTGGG GCCTCGGGTC
101   AGTTCGAGTT GGAGATCCTG TCCATGCAGA ACGTGAACGG GGAGCTGCAG
151   AACGGGAACT GCTGCGGCGG CGCCCGGAAC CCGGGAGACC GCAAGTGCAC
201   CCGCGACGAG TGTGACACAT ACTTCAAAGT GTGCCTCAAG GAGTATCAGT
251   CCCGCGTCAC GGCCGGGGGG CCCTGCAGCT TCGGCTCAGG GTCCACGCCT
301   GTCATCGGGG GCAACACCTT CAACCTCAAG GCCAGCCGCG GCAACGACCG
351   CAACCGCATC GTGCTGCCTT TCAGTTTCGC CTGGCCGAGG TCCTATACGT
401   TGCTTGTGGA GGCGTGGGAT TCCAGTAATG ACACCGTTCA ACCTGACAGT
451   ATTATTGAAA AGGCTTCTCA CTCGGGCATG ATCAACCCCA GCCGGCAGTG
501   GCAGACGCTG AAGCAGAACA CGGGCGTTGC CCACTTTGAG TATCAGATCC
551   GCGTGACCTG TGATGACTAC TACTATGGCT TTGGCTGYAA TAAGTTCTGC
601   CGCCCCAGAG ATGACTTCTT TGGACACTAT GCCTGTGACC AGAATGGCAA
651   CAAAACTTGC ATGGAAGGCT GGATGGGCCC CGAATGTAAC AGAGCTATTT
701   GCCGACAAGG CTGCAGTCCT AAGCATGGGT CTTGCAAACT CCCAGGTGAC
751   TGCAGGTGCC AGTAYGGCTG GCAAGGCCTG TACTGTGATA AGTGCATCCC
801   ACACCCGGGA TGCGTCCACG GCATCTGTAA TGAGCCCTGG CAGTGCCTCT
851   GTGAGACCAA CTGGGGCGGC CAGCTCTGTG ACAAAGATCT CAATTACTGT
901   GGGACTCATC AGCCGTGTCT CAACGGGGGA ACTTGTAGCA ACACAGGCCC
951   TGACAAATAT CAGTGTTCCT GCCCTGAGGG GTATTCAGGA CCCAACTGTG
1001  AAATTGCTGA GCACGCCTGC CTCTCTGATC CCTGTCACAA CAGAGGCAGC
1051  TGTAAGGAGA CCTCCCTGGG CTTTGAGTGT GAGTGTTCCC CAGGCTGGAC
1101  CGGCCCCACA TGCTCTACAA ACATTGATGA CTGTTCTCCT AATAACTGTT
1151  CCCACGGGGG CACCTGCCAG GACCTGGTTA ACGGATTTAA GTGTGTGTGC
1201  CCCCCACAGT GGACTGGGAA AACGTGCCAG TTAGATGCAA ATGAATGTGA
1251  GGCCAAACCT TGTGTAAACG CCAAATCCTG TAAGAATCTC ATTGCCAGCT
1301  ACTACTGCGA CTGTCTTCCC GGCTGGATGG GTCAGAATTG TGACATAAAT
1351  ATTAATGACT GCCTTGGCCA GTGTCAGAAT GACGCCTCCT GTCGGGATTT
1401  GGTTAATGGT TATCGCTGTA TCTGTCCACC TGGCTATGCA GGCGATCACT
1451  GTGAGAGAGA CATCGATGAA TGTGCCAGCA ACCCCTGTTT GAATGGGGGT
1501  CACTGTCAGA ATGAAATCAA CAGATTCCAG TGTCTGTGTC CCACTGGTTT
1551  CTCTGGAAAC CTCTGTCAGC TGGACATCGA TTATTGTGAG CCTAATCCCT
1601  GCCAGAACGG TGCCCAGTGC TACAACCGTG CCAGTGACTA TTTCTGCAAG
1651  TGCCCCGAGG ACTATGAGGG CAAGAACTGC TCACACCTGA AAGACCACTG
1701  CCGCACGACC CCCTGTGAAG TGATTGACAG CTGCACAGTG GCCATGGCTT
1751  CCAACGACAC ACCTGAAGGG GTGCGGTATA TTTCCTCCAA CGTCTGTGGT
1801  CCTCACGGGA AGTGCAAGAG TCAGTCGGGA GGCAAATTCA CCTGTGACTG
1851  TAACAAAGGC TTCACGGGAA CATACTGCCA TGAAAATATT AATGACTGTG
1901  AGAGCAACCC TTGTAGAAAC GGTGGCACTT GCATCGATGG TGTCAACTCC
1951  TACAAGTGCA TCTGTAGTGA CGGCTGGGAG GGGGCCTACT GTGAAACCAA
2001  TATTAATGAC TGCAGCCAGA ACCCCTGCCA CAATGGGGGC ACGTGTCGCG
```

FIG. 8B

```
2051 ACCTGGTCAA TGACTTCTAC TGTGACTGTA AAAATGGGTG GAAAGGAAAG
2101 ACCTGCCACT CACGTGACAG TCAGTGTGAT GAGGCCACGT GCAACAACGG
2151 TGGCACCTGC TATGATGAGG GGGATGCTTT TAAGTGCATG TGTCCTGGCG
2201 GCTGGGAAGG AACAACCTGT AACATAGCCC GAAACAGTAG CTGCCTGCCC
2251 AACCCCTGCC ATAATGGGGG CACATGTGTG GTCAACGGCG AGTCCTTTAC
2301 GTGCGTCTGC AAGGAAGGCT GGGAGGGGCC CATCTGTGCT CAGAATACCA
2351 ATGACTGCAG CCCTCATCCC TGTTACAACA GCGGCACCTG TGTGGATGGA
2401 GACAACTGGT ACCGGTGCGA ATGTGCCCCG GGTTTTGCTG GGCCCGACTG
2451 CAGAATAAAC ATCAATGAAT GCCAGTCTTC ACCTTGTGCC TTTGGAGCGA
2501 CCTGTGTGGA TGAGATCAAT GGCTACCGGT GTGTCTGCCC TCCAGGGCAC
2551 AGTGGTGCCA AGTGCCAGGA AGTTTCAGGG AGACCTTGCA TCACCATGGG
2601 GAGTGTGATA CCAGATGGGG CCAAATGGGA TGATGACTGT AATACCTGCC
2651 AGTGCCTGAA TGGACGGATC GCCTGCTCAA AGGTCTGGTG TGGCCCTCGA
2701 CCTTGCCTGC TCCACAAAGG GCACAGCGAG TGCCCCAGCG GGCAGAGCTG
2751 CATCCCCATC CTGGACGACC AGTGCTTCGT CCACCCCTGC ACTGGTGTGG
2801 GCGAGTGTCG GTCTTCCAGT CTCCAGCCGG TGAAGACAAA GTGCACCTCT
2851 GACTCCTATT ACCAGGATAA CTGTGCGAAC ATCACATTTA CCTTTAACAA
2901 GGAGATGATG TCACCAGGTC TTACTACGGA GCACATTTGC AGTGAATTGA
2951 GGAATTTGAA TATTTTGAAG AATGTTTCCG CTGAATATTC AATCTACATC
3001 GCTTGCGAGC CTTCCCCTTC AGCGAACAAT GAAATACATG TGGCCATTTC
3051 TGCTGAAGAT ATACGGGATG ATGGGAACCC GATCAAGGAA ATCACTGACA
3101 AAATAATCGA TCTTGTTAGT AAACGTGATG GAAACAGCTC GCTGATTGCT
3151 GCCGTTGCAG AAGTAAGAGT TCAGAGGCGG CCTCTGAAGA ACAGAACAGA
3201 TTTCCTTGTT CCCTTGCTGA GCTCTGTCTT AACTGTGGCT TGGATCTGTT
3251 GCTTGGTGAC GGCCTTCTAC TGGTGCCTGC GGAAGCGGCG GAAGCCGGGC
3301 AGCCACACAC ACTCAGCCTC TGAGGACAAC AECCACCAACA ACGTGCGGGA
3351 GCAGCTGAAC CAGATCAAAA ACCCCATTGA GAAACATGGG GCCAACACGG
3401 TCCCCATCAA GGATTACGAG AACAAGAACT CCAAAATGTC TAAAATAAGG
3451 ACACACAATT CTGAAGTAGA AGAGGACGAC ATGGACAAAC ACCAGCAGAA
3501 AGCCCGGTTT GGCAAGCAGC CGGCGTATAC GCTGGTAGAC AGAGAAGAGA
3551 AGCCCCCCAA CGGCACGCCG ACAAAACACC CAAACTGGAC AAACAAACAG
3601 GACAACAGAG ACTTGGAAAG TGCCCAGAGC TTAAACCGAA TGGAGTACAT
3651 CGTATAG
```

FIG. 8C

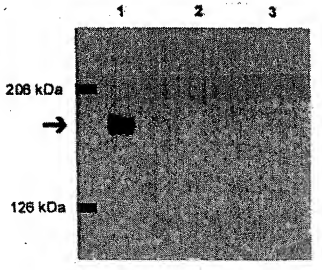


FIG. 9

FIG. 10A

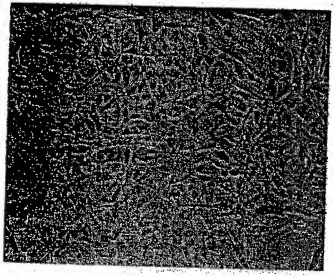


FIG. 10C

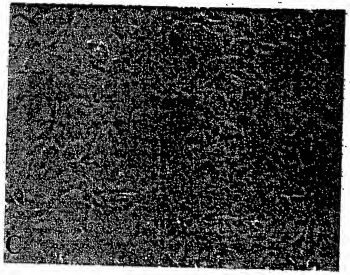
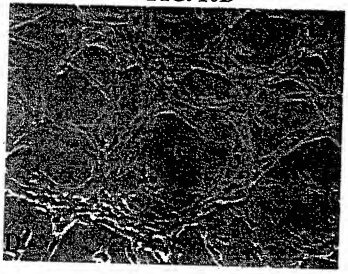


FIG. 10B

FIG. 10D



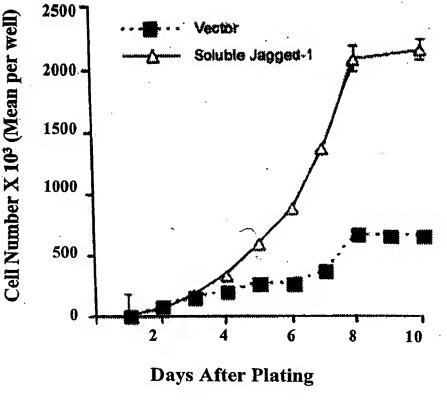

Vector
Soluble Jagged-1
Cell Number X 10³ (Mean per well)
2500
2000
1500
1000
500
0
2
4
6
8
10
Days After Plating

FIG. 11

FIG. 12A

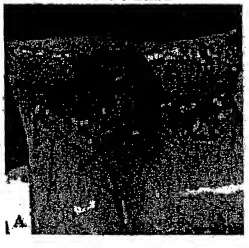


FIG. 12B

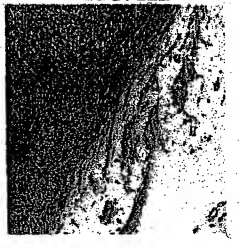


FIG. 12C

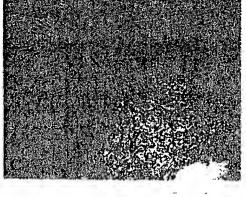


FIG. 12D

```
1    MRSPRTRGRS RPLSLLLALL CALRAKVCGA SGQFELEILS MQNVNGELQN
51   GNCCGGARNP GDRKCTRDEC DTYFKVCLKE YQSRVTAGGP CSFGSGSTPV
101  IGGNTFNLKA SRGNDRNRIV LPFSFAWPRS YTLLVEAWDS SNDTVQPDSI
151  IEKASHSGMI NPSRQWQTLK QNTGVAHFEY QIRVTCDDYY YGFGCNKFCR
201  PRDDFFGHYA CDQNGNKTCM EGWMGPECNR AICRQGCSPK HGSCKLPGDC
251  RCQYGWQGLY CDKCIPHPGC VHGICNEPWQ CLCETNWGGQ LCDKDLNYCG
301  THQPCLNGGT CSNTGPDKYQ CSCPEGYSGP NCEIAEHACL SDPCHNRGSC
351  KETSLGFECE CSPGWTGPTC STNIDDCSPN NCSHGGTCQD LVNGFKCVCP
401  PQWTGKTCQL DANECEAKPC VNAKSCKNLI ASYYCDCLPG WMGQNCDINI
451  NDCLGQCQND ASCRDLVNGY RCICPPGYAG DHCERDIDEC ASNPCLNGGH
501  CQNEINRFQC LCPTGFSGNL CQLDIDYCEP NPCQNGAQCY NRASDYFCKC
551  PEDYEGKNCS HLKDHCRTTP CEVIDSCTVA MASNDTPEGV RYISSNVCGP
601  HGKCKSQSGG KFTCDCNKGF TGTYCHENIN DCESNPCRNG GTCIDGVNSY
651  CICSDGWEGA YCETNINDCS QNPCHNGGTC RDLVNDFYCD CKNGWKGKTC
701  HSRDSQCDEA TCNNGGTCYD EGDAFKCMCP GGWEGTTCNI ARNSSCLPNP
751  CHNGGTCVVN GESFTCVCKE GWEGPICAQN TNDCSPHPCY NSGTCVDGDN
801  WYRCECAPGF AGPDCRININ ECQSSPCAFG ATCVDEINGY RCVCPPGHSG
851  AKCQEVSGRP CITMGSVIPD GAKWDDDCNT CQCLNGRIAC SKVWCGPRPC
901  LLHKGHSECP SGQSCIPILD DQCFVHPCTG VGECRSSSLQ PVKTKCTSDS
951  YYQDNCANIT FTFNKEMMSP GLTTEHICSE LRNLNILKNV SAEYSIYIAC
1001 EPSPSANNEI HVAISAEDIR DDGNPIKEIT DKIIDLVSKR DGNSSLIAAV
1051 AEVRVQRRPL KNRTD
```

FIG. 13A

```
1     ATGCGTTCCC CACGGACRCG CGGCCGGTCC GGGCGCCCCC TAAGCCTCCT
51    GCTCGCCCTG CTCTGTGCCC TGCGAGCCAA GGTGTGTGGG GCCTCGGGTC
101   AGTTCGAGTT GGAGATCCTG TCCATGCAGA ACGTGAACGG GGAGCTGCAG
151   AACGGGAACT GCTGCGGCGG CGCCCGGAAC CCGGGAGACC GCAAGTGCAC
201   CCGCGACGAG TGTGACACAT ACTTCAAAGT GTGCCTCAAG GAGTATCAGT
251   CCCGCGTCAC GGCCGGGGGG CCCTGCAGCT TCGGCTCAGG GTCCACGCCT
301   GTCATCGGGG GCAACACCTT CAACCTCAAG GCCAGCCGCG GCAACGACCG
351   CAACCGCATC GTGCTGCCTT TCAGTTTCGC CTGGCCGAGG TCCTATACGT
401   TGCTTGTGGA GGCGTGGGAT TCCAGTAATG ACACCGTTCA ACCTGACAGT
451   ATTATTGAAA AGGCTTCTCA CTCGGGCATG ATCAACCCCA GCCGGCAGTG
501   GCAGACGCTG AAGCAGAACA CGGGCGTTGC CCACTTTGAG TATCAGATCC
551   GCGTGACCTG TGATGACTAC TACTATGGCT TTGGCTGYAA TAAGTTCTGC
601   CGCCCCAGAG ATGACTTCTT TGGACACTAT GCCTGTGACC AGAATGGCAA
651   CAAAACTTGC ATGGAAGGCT GGATGGGCCC CGAATGTAAC AGAGCTATTT
701   GCCGACAAGG CTGCAGTCCT AAGCATGGGT CTTGCAAACT CCCAGGTGAC
751   TGCAGGTGCC AGTAYGGCTG GCAAGGCCTG TACTGTGATA AGTGCATCCC
801   ACACCCGGGA TGCGTCCACG GCATCTGTAA TGAGCCCTGG CAGTGCCTCT
851   GTGAGACCAA CTGGGGCGGC CAGCTCTGTG ACAAAGATCT CAATTACTGT
901   GGGACTCATC AGCCGTGTCT CAACGGGGGA ACTTGTAGCA ACACAGGCCC
951   TGACAAATAT CAGTGTTCCT GCCCTGAGGG GTATTCAGGA CCCAACTGTG
1001  AAATTGCTGA GCACGCCTGC CTCTCTGATC CCTGTCACAA CAGAGGCAGC
1051  TGTAAGGAGA CCTCCCTGGG CTTTGAGTGT GAGTGTTCCC CAGGCTGGAC
1101  CGGCCCCACA TGCTCTACAA ACATTGATGA CTGTTCTCCT AATAACTGTT
1151  CCCACGGGGG CACCTGCCAG GACCTGGTTA ACGGATTTAA GTGTGTGTGC
1201  CCCCCACAGT GGACTGGGAA AACGTGCCAG TTAGATGCAA ATGAATGTGA
1251  GGCCAAACCT TGTGTAAACG CCAAATCCTG TAAGAATCTC ATTGCCAGCT
1301  ACTACTGCGA CTGTCTTCCC GGCTGGATGG GTCAGAATTG TGACATAAAT
1351  ATTAATGACT GCCTTGGCCA GTGTCAGAAT GACGCCTCCT GTCGGGATTT
1401  GGTTAATGGT TATCGCTGTA TCTGTCCACC TGGCTATGCA GGCGATCACT
1451  GTGAGAGAGA CATCGATGAA TGTGCCAGCA ACCCCTGTTT GAATGGGGGT
```

FIG. 13B

```
1501 CACTGTCAGA ATGAAATCAA CAGATTCCAG TGTCTGTGTC CCACTGGTTT
1551 CTCTGGAAAC CTCTGTCAGC TGGACATCGA TTATTGTGAG CCTAATCCCT
1601 GCCAGAACGG TGCCCAGTGC TACAACCGTG CCAGTGACTA TTTCTGCAAG
1651 TGCCCCGAGG ACTATGAGGG CAAGAACTGC TCACACCTGA AAGACCACTG
1701 CCGCACGACC CCCTGTGAAG TGATTGACAG CTGCACAGTG GCCATGGCTT
1751 CCAACGACAC ACCTGAAGGG GTGCGGTATA TTTCCTCCAA CGTCTGTGGT
1801 CCTCACGGGA AGTGCAAGAG TCAGTCGGGA GGCAAATTCA CCTGTGACTG
1851 TAACAAAGGC TTCACGGGAA CATACTGCCA TGAAAATATT AATGACTGTG
1901 AGAGCAACCC TTGTAGAAAC GGTGGCACTT GCATCGATGG TGTCAACTCC
1951 TACAAGTGCA TCTGTAGTGA CGGCTGGGAG GGGGCCTACT GTGAAACCAA
2001 TATTAATGAC TGCAGCCAGA ACCCCTGCCA CAATGGGGGC ACGTGTCGCG
2051 ACCTGGTCAA TGACTTCTAC TGTGACTGTA AAAATGGGTG GAAAGGAAAG
2101 ACCTGCCACT CACGTGACAG TCAGTGTGAT GAGGCCACGT GCAACAACGG
2151 TGGCACCTGC TATGATGAGG GGGATGCTTT TAAGTGCATG TGTCCTGGCG
2201 GCTGGGAAGG AACAACCTGT AACATAGCCC GAAACAGTAG CTGCCTGCCC
2251 AACCCCTGCC ATAATGGGGG CACATGTGTG GTCAACGGCG AGTCCTTTAC
2301 GTGCGTCTGC AAGGAAGGCT GGGAGGGGCC CATCTGTGCT CAGAATACCA
2351 ATGACTGCAG CCCTCATCCC TGTTACAACA GCGGCACCTG TGTGGATGGA
2401 GACAACTGGT ACCGGTGCGA ATGTGCCCCG GGTTTTGCTG GGCCCGACTG
2451 CAGAATAAAC ATCAATGAAT GCCAGTCTTC ACCTTGTGCC TTTGGAGCGA
2501 CCTGTGTGGA TGAGATCAAT GGCTACCGGT GTGTCTGCCC TCCAGGGCAC
2551 AGTGGTGCCA AGTGCCAGGA AGTTTCAGGG AGACCTTGCA TCACCATGGG
2601 GAGTGTGATA CCAGATGGGG CCAAATGGGA TGATGACTGT AATACCTGCC
2651 AGTGCCTGAA TGGACGGATC GCCTGCTCAA AGGTCTGGTG TGGCCCTCGA
2701 CCTTGCCTGC TCCACAAAGG GCACAGCGAG TGCCCCAGCG GGCAGAGCTG
2751 CATCCCCATC CTGGACGACC AGTGCTTCGT CCACCCCTGC ACTGGTGTGG
2801 GCGAGTGTCG GTCTTCCAGT CTCCAGCCGG TGAAGACAAA GTGCACCTCT
2851 GACTCCTATT ACCAGGATAA CTGTGCGAAC ATCACATTTA CCTTTAACAA
2901 GGAGATGATG TCACCAGGTC TTACTACGGA GCACATTTGC AGTGAATTGA
2951 GGAATTTGAA TATTTTGAAG AATGTTTCCG CTGAATATTC AATCTACATC
3001 GCTTGCGAGC CTTCCCCTTC AGCGAACAAT GAAATACATG TGGCCATTTC
3051 TGCTGAAGAT ATACGGGATG ATGGGAACCC GATCAAGGAA ATCACTGACA
3101 AAATAATCGA TCTTGTTAGT AAACGTGATG GAAACAGCTC GCTGATTGCT
3151 GCCGTTGCAG AAGTAAGAGT TCAGAGGCGG CCTCTGAAGA ACAGAACAGA
3201 T
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FIG. 13C